

Rec'd PCT/PTO 25 JUL 2005

10/506796

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/506,796A

Source: PU/10

Date Processed by STIC: 7/25/05

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RAW SEQUENCE LISTING

DATE: 07/25/2005

PATENT APPLICATION: US/10/506,796A

TIME: 08:55:16

Input Set : A:\012310006U2.txt

Output Set: N:\CRF4\07252005\J506796A.raw

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3 <110> APPLICANT: MOR, Tsafirir
4     MATOBA, Nobuyuki
5     ARNTZEN, Charles
7 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
9 <130> FILE REFERENCE: 01231.0006U2
11 <140> CURRENT APPLICATION NUMBER: 10/506,796A
12 <141> CURRENT FILING DATE: 2004-09-03
14 <150> PRIOR APPLICATION NUMBER: PCT/US03/07073
15 <151> PRIOR FILING DATE: 2003-03-06
17 <150> PRIOR APPLICATION NUMBER: 60/362,247
18 <151> PRIOR FILING DATE: 2002-03-06
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 35
26 <212> TYPE: PRT
27 <213> ORGANISM: Human immunodeficiency virus type 1
30 <220> FEATURE:
31 <221> NAME/KEY: PEPTIDE
32 <222> LOCATION: (1)..(35)
33 <223> OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
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39 Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp
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41 Tyr Ile Lys
42           35
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 6
47 <212> TYPE: PRT
48 <213> ORGANISM: Human immunodeficiency virus type 1
51 <220> FEATURE:
52 <221> NAME/KEY: PEPTIDE
53 <222> LOCATION: (1)..(6)
54 <223> OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 663-668)
56 <400> SEQUENCE: 2
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62 <210> SEQ ID NO: 3
63 <211> LENGTH: 36
64 <212> TYPE: PRT
65 <213> ORGANISM: Human immunodeficiency virus type 1

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70 1          5          10          15
71 Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu
72          20          25          30
73 Trp Tyr Ile Lys
74          35
77 <210> SEQ ID NO: 4
78 <211> LENGTH: 36
79 <212> TYPE: PRT
80 <213> ORGANISM: Human immunodeficiency virus type 1
83 <220> FEATURE:
84 <221> NAME/KEY: PEPTIDE
85 <222> LOCATION: (1)..(35)
86 <223> OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
88 <400> SEQUENCE: 4
90 Ser Gln Thr Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Gly Leu Asp
91 1          5          10          15
92 Lys Trp Glu Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp
93          20          25          30
94 Tyr Ile Lys Ile
95          35
98 <210> SEQ ID NO: 5
99 <211> LENGTH: 36
100 <212> TYPE: PRT
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104 <220> FEATURE:
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106 <222> LOCATION: (1)..(36)
107 <223> OTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
109 <400> SEQUENCE: 5
111 Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp
112 1          5          10          15
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114          20          25          30
115 Tyr Ile Lys Ile
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120 <211> LENGTH: 36
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125 <220> FEATURE:
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128 <223> OTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
130 <400> SEQUENCE: 6
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136 Tyr Ile Lys Ile
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149 <223> OTHER INFORMATION: HIV-1 isolate 1924v3.20 (residues 649-685)
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155 Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp Leu Trp
156          20          25          30
157 Tyr Ile Lys Ile
158          35
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 522
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Description of Artificial Sequence; note = synthetic
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169 <400> SEQUENCE: 8
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171 cacatggcac cccacaaaac atcactgact tgtgtgctga gtaccacaac acccaaatcc      120
172 acaaccctca atgacaagat ctttagctac accgagagcc ttgctggcaa gagggagatg      180
173 gctatcatcc cttcaagaat ggtgctacct tccaagtgga ggtgcctgga agccaacaca      240
174 ttgatagcca aaagaaggcc attgagagga tgaaggacac attaggatag cttacctcac      300
175 tgaggctaag gtggagaagc tttgtgtgtg gaacaacaag actccacatg ctattgctgc      360
176 cattagcatg gcaaattggtc ctggaccttc ccaaacccaa caagagaaga atgagcaaga      420
177 gcttttggag ttggacaagt ggcaagcctt tggaattggt ttgacatcac caattggctt      480
178 tggatatatca agatctctga gaaggatgaa ctctaagagc tc      522
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182 <211> LENGTH: 171
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence; note = synthetic
construct
189 <400> SEQUENCE: 9
191 Met Ala Ile Lys Leu Lys Phe Gly Val Phe Phe Thr Val Leu Leu Ser
192 1          5          10          15
193 Ser Ala Trp Ala His Gly Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala
194          20          25          30
195 Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser
196          35          40          45
197 Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe
198          50          55          60

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199 Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile
200 65                      70                      75                      80
201 Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile
202                      85                      90                      95
203 Ala Thr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn
204                      100                      105                      110
205 Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn Gly Pro Gly
206                      115                      120                      125
207 Pro Ser Gln Thr Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu
208                      130                      135                      140
209 Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu
210 145                      150                      155                      160
211 Trp Tyr Ile Lys Ile Ser Glu Lys Asp Glu Leu
212                      165                      170

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